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1645

TECH CENTER 1600/2900

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/121,587A

DATE: 12/08/2000

TIME: 10:20:09

Input Set : A:\06132.033003.SEQLIST.TXT

Output Set: N:\CRF3\12082000\I121587A.raw

4 <110> APPLICANT: Chambers, Thomas J.  
 5 Guirakhoo, Farshad  
 6 Monath, Thomas P.  
 8 <120> TITLE OF INVENTION: CHIMERIC FLAVIVIRUS VACCINES  
 11 <130> FILE REFERENCE: 06132/033003  
 13 <140> CURRENT APPLICATION NUMBER: 09/121,587A  
 14 <141> CURRENT FILING DATE: 1998-07-23  
 16 <150> PRIOR APPLICATION NUMBER: US98/03894  
 17 <151> PRIOR FILING DATE: 1998-03-02  
 19 <150> PRIOR APPLICATION NUMBER: 09/007,664  
 20 <151> PRIOR FILING DATE: 1998-01-15  
 22 <150> PRIOR APPLICATION NUMBER: 08/807,445  
 23 <151> PRIOR FILING DATE: 1997-02-28  
 25 <160> NUMBER OF SEQ ID NOS: 29  
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 1983  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Dengue-2 virus  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: CDS  
 36 <222> LOCATION: (1)...(1983)  
 38 <400> SEQUENCE: 1  
 39 ttc cat cta acc aca cgt aac gga gaa cca cac atg atc gtc agt aga 48  
 40 Phe His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg  
 41 1 5 10 15  
 43 caa gag aaa ggg aaa agt ctt ttg ttt aaa aca gag gat ggc gtg aac 96  
 44 Gln Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Glu Asp Gly Val Asn  
 45 20 25 30  
 47 atg tgc acc ctc atg gcc atg gac ctt ggt gaa ttg tgt gaa gac aca 144  
 48 Met Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr  
 49 35 40 45  
 51 atc acg tac aag tgt ccc ctt ctc agg cag aat gag cca gaa gac ata 192  
 52 Ile Thr Tyr Lys Cys Pro Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile  
 53 50 55 60  
 55 gac tgc tgg tgc aac tcc acg tcc acg tgg gta acc tat ggg act tgt 240  
 56 Asp Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys  
 57 65 70 75 80  
 59 acc acc acg gga gaa cat aga aga gaa aaa aga tca gtg gca ctc gtt 288  
 60 Thr Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val  
 61 85 90 95  
 63 cca cat gtg gga atg gga ctg gag acg cga act gaa aca tgg atg tca 336  
 64 Pro His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser  
 65 100 105 110  
 67 tca gaa ggg gct tgg aaa cat gcc cag aga att gaa att tgg atc ctg 384  
 68 Ser Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Ile Trp Ile Leu  
 69 115 120 125

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71 aga cat cca ggc ttc acc ata atg gca gca atc ctg gca tac acc ata 432
72 Arg His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile
73 130 135 140
75 ggg acg aca cat ttc cag aga gca ctg att ttc atc tta ctg aca gct 480
76 Gly Thr Thr His Phe Gln Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala
77 145 150 155 160
79 gtc gct cct tca atg aca atg cgt tgc ata gga ata tca aat aga gac 528
80 Val Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp
81 165 170 175
83 ttt gta gaa ggg gtt tca gga gga agc tgg gtt gac ata gtc tta gaa 576
84 Phe Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu
85 180 185 190
87 cat gga agc tgt gtg acg acg atg gca aaa aac aaa cca aca ttg gat 624
88 His Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
89 195 200 205
91 ttt gaa ctg ata aaa aca gaa gcc aaa cag cct gcc acc cta agg aag 672
92 Phe Glu Leu Ile Lys Thr Thr Met Ala Lys Gln Pro Ala Thr Leu Arg Lys
93 210 215 220
95 tac tgt ata gag gca aag cta acc aac aca aca aca gaa tct cgt tgc 720
96 Tyr Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys
97 225 230 235 240
99 cca aca caa ggg gaa ccc agc cta aat gaa gag cag gat aaa agg ttc 768
100 Pro Thr Gln Gly Glu Pro Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe
101 245 250 255
103 gtc tgc aaa cac tcc atg gta gac aga gga tgg gga aat gga tgt gga 816
104 Val Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
105 260 265 270
107 tta ttt gga aag gga ggc att gtg acc tgt gct atg ttc aca tgc aaa 864
108 Leu Phe Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys
109 275 280 285
111 aag aac atg gag gga aaa gtt gtg cag cca gaa aac ttg gaa tac acc 912
112 Lys Asn Met Glu Gly Lys Val Val Gln Pro Glu Asn Leu Glu Tyr Thr
113 290 295 300
115 att gtg gta aca ccc cac tca ggg gaa gag cat gcg gtc gga aat gac 960
116 Ile Val Val Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp
117 305 310 315 320
119 aca gga aaa cat ggc aag gaa atc aaa gta aca cca cag agt tcc atc 1008
120 Thr Gly Lys His Gly Lys Glu Ile Lys Val Thr Pro Gln Ser Ser Ile
121 325 330 335
123 aca gaa gca gaa ttg aca ggt tat ggc act gtc acg atg gag tgc tct 1056
124 Thr Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser
125 340 345 350
127 ccg aga aca ggc ctc gac ttc aat gag atg gtg ttg ctg cag atg gaa 1104
128 Pro Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Glu
129 355 360 365
131 aat aaa gct tgg ctg gtg cat agg caa tgg ttc cta gac ctg ccg tta 1152
132 Asn Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu
133 370 375 380
135 cca tgg ctg ccc gga gcg gac aca caa ggg tca aat tgg ata caa aaa 1200

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136 Pro Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys
137 385 390 395 400
139 gaa aca ttg gtc act ttc aaa aat cct cat gcg aag aaa cag gat gtt 1248
140 Glu Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val
141 405 410 415
143 gtt gtt tta gga tcc caa gaa ggg gcc atg cac aca gca ctc aca ggg 1296
144 Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly
145 420 425 430
147 gcc aca gaa atc caa atg tca tca gga aac tta ctc ttc aca gga cat 1344
148 Ala Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His
149 435 440 445
151 ctc aag tgc agg ctg aga atg gac aag cta caq ctc aaa gga atg tca 1392
152 Leu Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser
153 450 455 460
155 tac tct atg tgc aca gga aag ttt aaa gtt gtg aag gaa ata gca gaa 1440
156 Tyr Ser Met Cys Thr Gly Lys Phe Lys Val Val Lys Glu Ile Ala Glu
157 465 470 475 480
159 aca caa cat gga aca ata gtt atc agg gtg cag tat gaa ggg gac ggc 1488
160 Thr Gln His Gly Thr Ile Val Ile Arg Val Gln Tyr Glu Gly Asp Gly
161 485 490 495
163 tct cca tgt aaa atc cct ttt gag ata atg gat ttg gaa aaa aga cat 1536
164 Ser Pro Cys Lys Ile Pro Phe Glu Ile Met Asp Leu Glu Lys Arg His
165 500 505 510
167 gtc tta ggt cgc ctg atc aca gtc aac cca att gtg aca gaa aaa gat 1584
168 Val Leu Gly Arg Leu Ile Thr Val Asn Pro Ile Val Thr Glu Lys Asp
169 515 520 525
171 agc cca gtc aac ata gaa gca gaa cct cca ttc gga gac agc tac atc 1632
172 Ser Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile
173 530 535 540
175 atc ata gga gta gag cgg gga caa ctg aag ctc aac tgg ttt aag aaa 1680
176 Ile Ile Gly Val Glu Pro Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys
177 545 550 555 560
179 gga agt tct atc ggc caa atg ttt gag aca aca atg agg ggg gcg aag 1728
180 Gly Ser Ser Ile Gly Gln Met Phe Glu Thr Thr Met Arg Gly Ala Lys
181 565 570 575
183 aga atg gcc att ttg ggt gac aca gcc tgg gat ttt gga tcc ctg gga 1776
184 Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly
185 580 585 590
187 gga gtg ttt aca tct ata gga aaa gcc ctc cac caa gtc ttt gga gca 1824
188 Gly Val Phe Thr Ser Ile Gly Lys Ala Leu His Gln Val Phe Gly Ala
189 595 600 605
191 atc tat gga gct gcc ttc agt ggg gtc tca tgg act atg aaa atc ctc 1872
192 Ile Tyr Gly Ala Ala Phe Ser Gly Val Ser Trp Thr Met Lys Ile Leu
193 610 615 620
195 ata gga gtc att atc aca tgg ata gga atg aat tca cgc agc acc tca 1920
196 Ile Gly Val Ile Ile Thr Trp Ile Gly Met Asn Ser Arg Ser Thr Ser
197 625 630 635 640
199 ctg tct gtg tca cta gta ttg gtg gga gtc gtg acg ctg tat ttg gga 1968
200 Leu Ser Val Ser Leu Val Leu Val Gly Val Val Thr Leu Tyr Leu Gly

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201          645          650          655
203 gtt atg gtg ggc gcc 1983
204 Val Met Val Gly Ala
205          660
208 <210> SEQ ID NO: 2
209 <211> LENGTH: 661
210 <212> TYPE: PRT
211 <213> ORGANISM: Dengue-2 virus
213 <400> SEQUENCE: 2
214 Phe His Leu Thr Thr Arg Asn Gly Glu Pro His Met Ile Val Ser Arg
215 1 5 10 15
216 Gln Glu Lys Gly Lys Ser Leu Leu Phe Lys Thr Glu Asp Gly Val Asn
217 20 25 30
218 Met Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr
219 35 40 45
220 Ile Thr Tyr Lys Cys Pro Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile
221 50 55 60
222 Asp Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys
223 65 70 75 80
224 Thr Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val
225 85 90 95
226 Pro His Val Gly Met Gly Leu Glu Thr Arg Thr Glu Thr Trp Met Ser
227 100 105 110
228 Ser Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Ile Trp Ile Leu
229 115 120 125
230 Arg His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile
231 130 135 140
232 Gly Thr Thr His Phe Gln Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala
233 145 150 155 160
234 Val Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp
235 165 170 175
236 Phe Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu
237 180 185 190
238 His Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
239 195 200 205
240 Phe Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys
241 210 215 220
242 Tyr Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys
243 225 230 235 240
244 Pro Thr Gln Gly Glu Pro Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe
245 245 250 255
246 Val Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
247 260 265 270
248 Leu Phe Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys
249 275 280 285
250 Lys Asn Met Glu Gly Lys Val Val Gln Pro Glu Asn Leu Glu Tyr Thr
251 290 295 300
252 Ile Val Val Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp
253 305 310 315 320

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254 Thr Gly Lys His Gly Lys Glu Ile Lys Val Thr Pro Gln Ser Ser Ile
255                               325                               330                               335
256 Thr Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser
257                               340                               345                               350
258 Pro Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Glu
259                               355                               360                               365
260 Asn Lys Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu
261                               370                               375                               380
262 Pro Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys
263 385                               390                               395                               400
264 Glu Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val
265                               405                               410                               415
266 Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly
267                               420                               425                               430
268 Ala Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His
269                               435                               440                               445
270 Leu Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser
271                               450                               455                               460
272 Tyr Ser Met Cys Thr Gly Lys Phe Lys Val Val Lys Glu Ile Ala Glu
273 465                               470                               475                               480
274 Thr Gln His Gly Thr Ile Val Ile Arg Val Gln Tyr Glu Gly Asp Gly
275                               485                               490                               495
276 Ser Pro Cys Lys Ile Pro Phe Glu Ile Met Asp Leu Glu Lys Arg His
277                               500                               505                               510
278 Val Leu Gly Arg Leu Ile Thr Val Asn Pro Ile Val Thr Glu Lys Asp
279                               515                               520                               525
280 Ser Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile
281                               530                               535                               540
282 Ile Ile Gly Val Glu Pro Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys
283 545                               550                               555                               560
284 Gly Ser Ser Ile Gly Gln Met Phe Glu Thr Thr Met Arg Gly Ala Lys
285                               565                               570                               575
286 Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly
287                               580                               585                               590
288 Gly Val Phe Thr Ser Ile Gly Lys Ala Leu His Gln Val Phe Gly Ala
289                               595                               600                               605
290 Ile Tyr Gly Ala Ala Phe Ser Gly Val Ser Trp Thr Met Lys Ile Leu
291                               610                               615                               620
292 Ile Gly Val Ile Ile Thr Trp Ile Gly Met Asn Ser Arg Ser Thr Ser
293 625                               630                               635                               640
294 Leu Ser Val Ser Leu Val Leu Val Gly Val Val Thr Leu Tyr Leu Gly
295                               645                               650                               655
296 Val Met Val Gly Ala
297                               660
300 <210> SEQ ID NO: 3
301 <211> LENGTH: 7
302 <212> TYPE: PRT
303 <213> ORGANISM: Japanese Encephalitis virus
305 <400> SEQUENCE: 3

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VERIFICATION SUMMARY

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